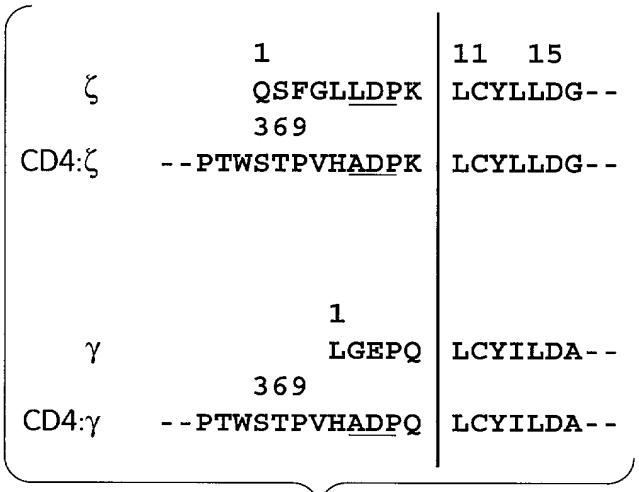
1
11 15
ζ QSFGLLDPK LCYLLDG--
369
CD4:ζ --PTWSTPVHADPK LCYLLDG--
1
γ LGEPQ LCYILDA--
369
CD4:γ --PTWSTPVHADPQ LCYILDA--

Fig. 1a

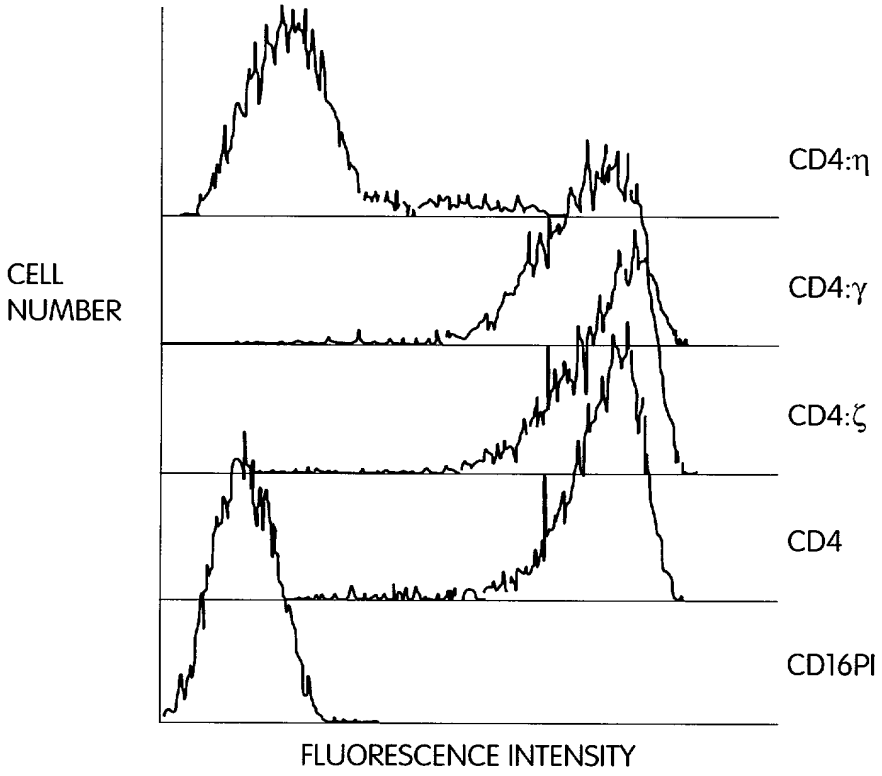
CELL NUMBER
CD4:η
CD4:γ
CD4:ζ
CD4
CD16PI
FLUORESCENCE INTENSITY

Fig. 1b

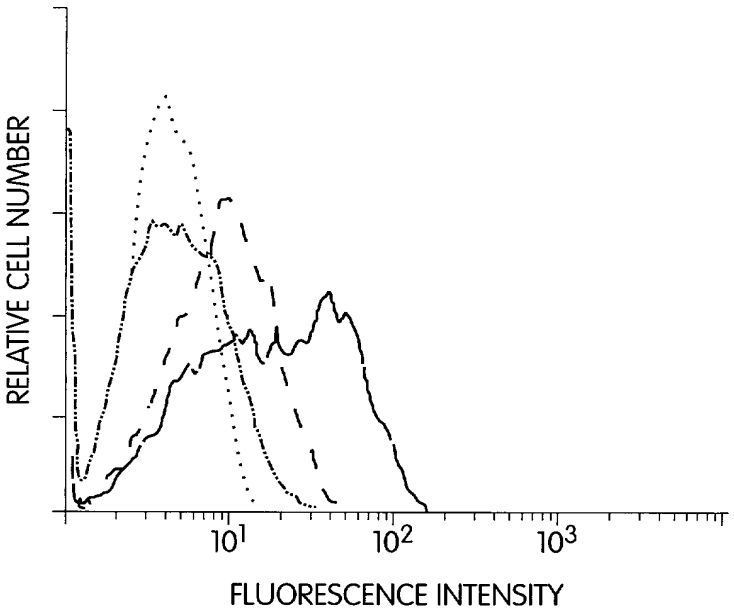
RELATIVE CELL NUMBER
10^1
10^2
10^3
FLUORESCENCE INTENSITY

Fig. 2

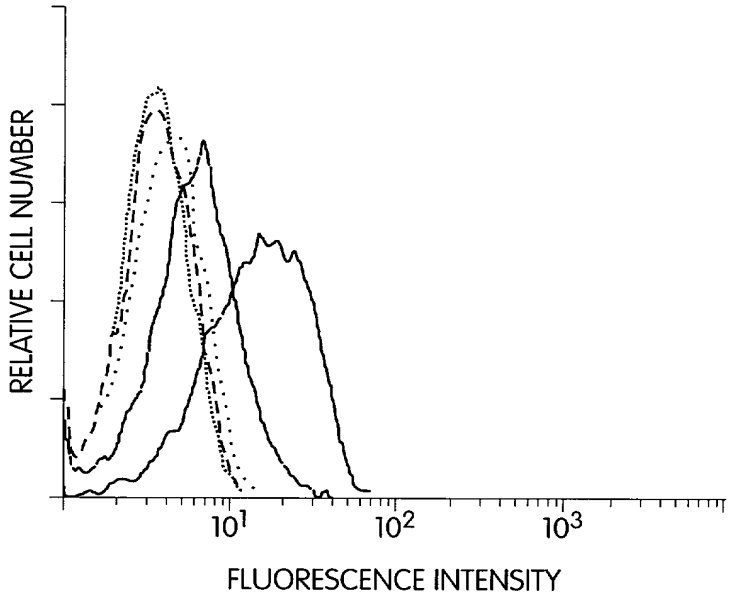
RELATIVE CELL NUMBER
10^1
10^2
10^3
FLUORESCENCE INTENSITY

Fig. 3

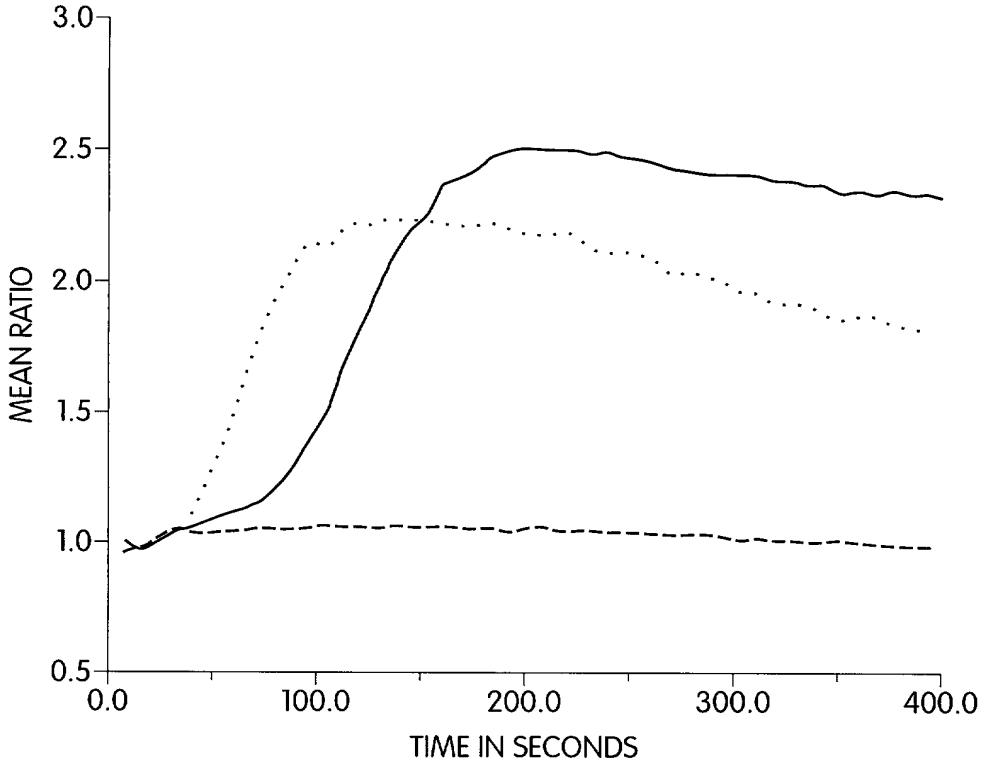
3.0
2.5
2.0
1.5
1.0
0.5
MEAN RATIO
0.0
100.0
200.0
300.0
400.0
TIME IN SECONDS

Fig. 4a

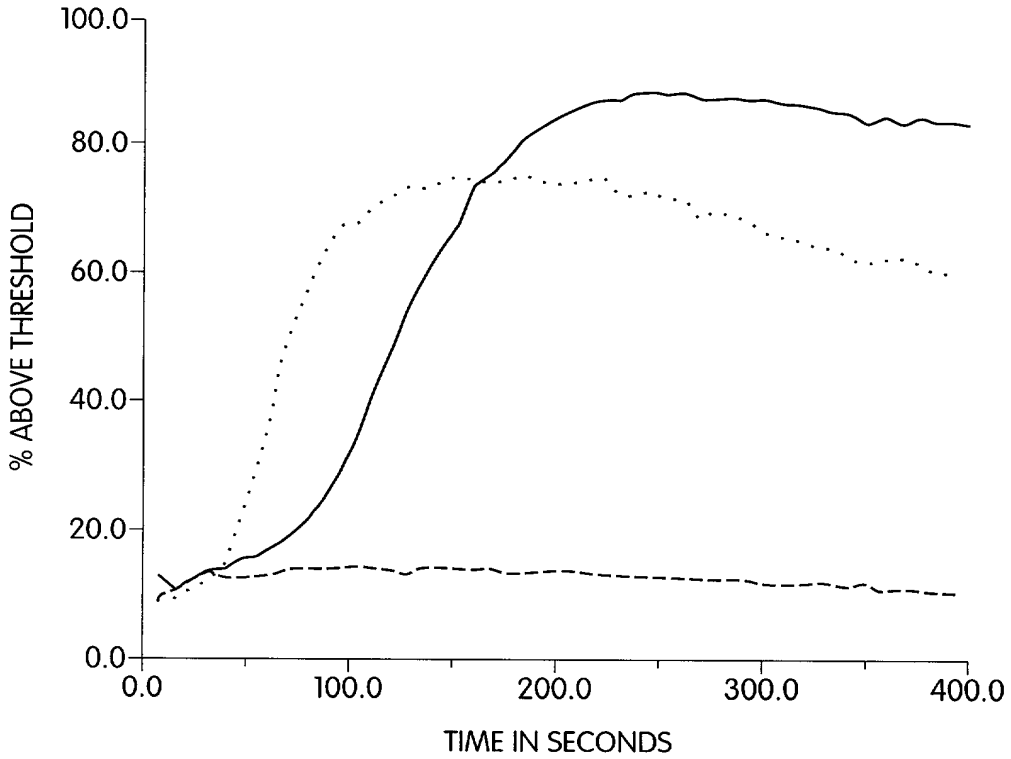
100.0
80.0
60.0
40.0
20.0
0.0
% ABOVE THRESHOLD
0.0
100.0
200.0
300.0
400.0
TIME IN SECONDS

Fig. 4b

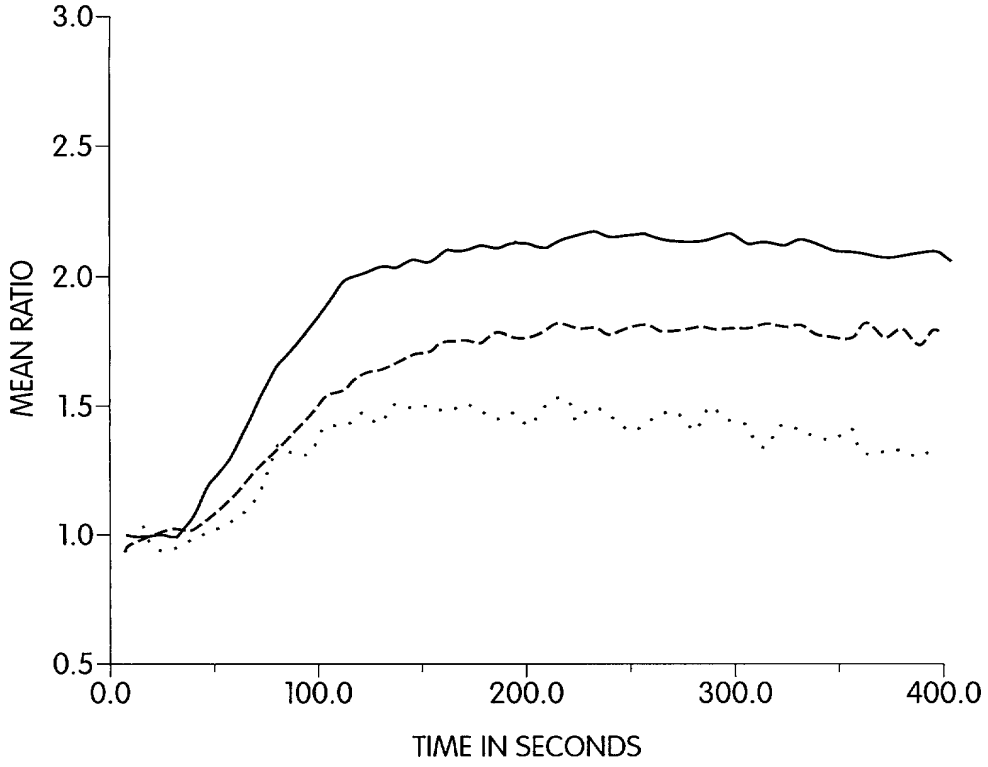
3.0
2.5
2.0
1.5
1.0
0.5
MEAN RATIO
0.0
100.0
200.0
300.0
400.0
TIME IN SECONDS

Fig. 4c

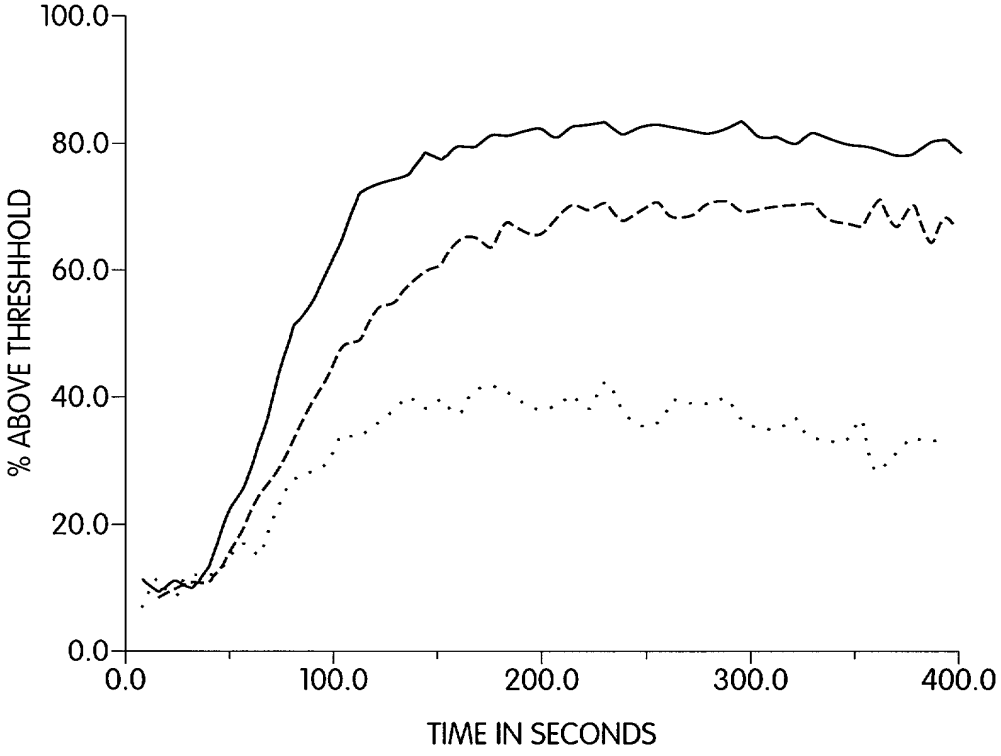
100.0
80.0
60.0
40.0
20.0
0.0
% ABOVE THRESHHOLD
0.0
100.0
200.0
300.0
400.0
TIME IN SECONDS

Fig. 4d

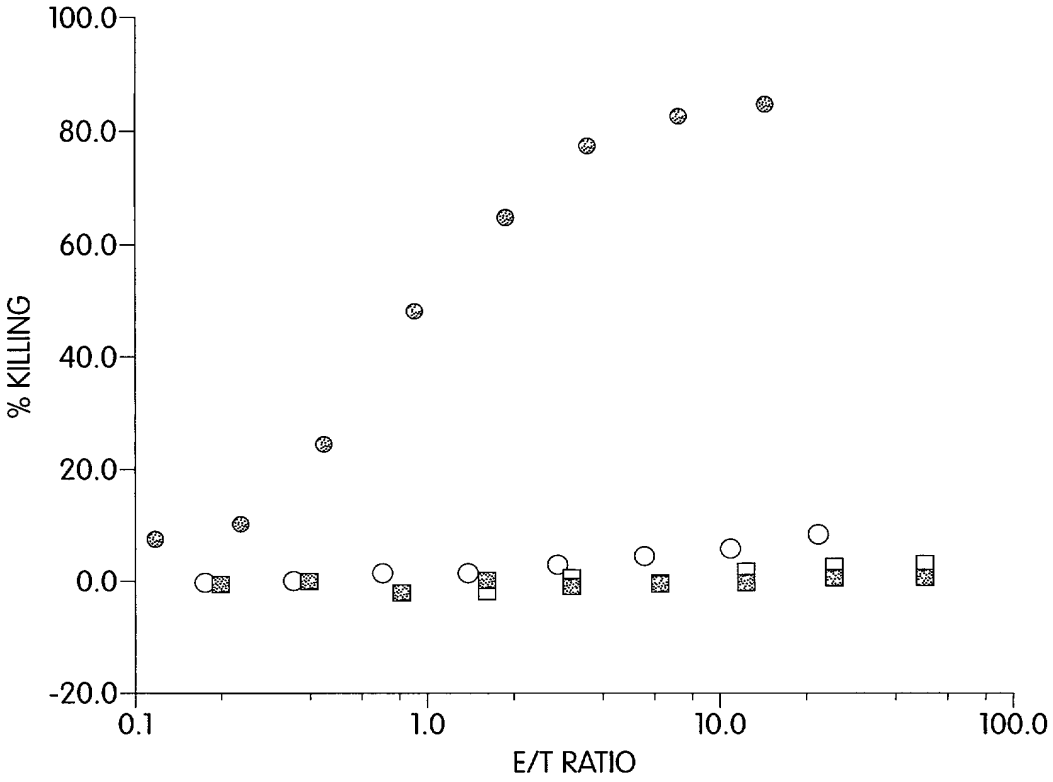
100.0
80.0
60.0
40.0
20.0
0.0
-20.0
% KILLING
0.1
1.0
10.0
100.0
E/T RATIO

Fig. 5a

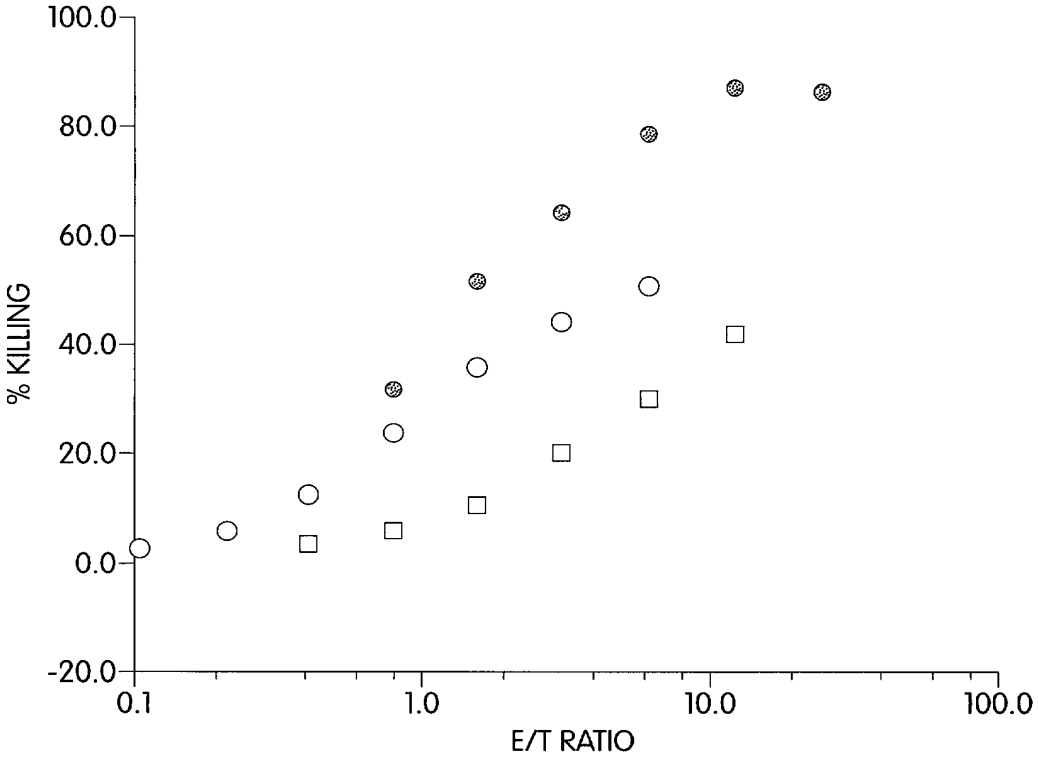
100.0
80.0
60.0
40.0
20.0
0.0
-20.0
% KILLING
0.1
1.0
10.0
100.0
E/T RATIO

Fig. 5b

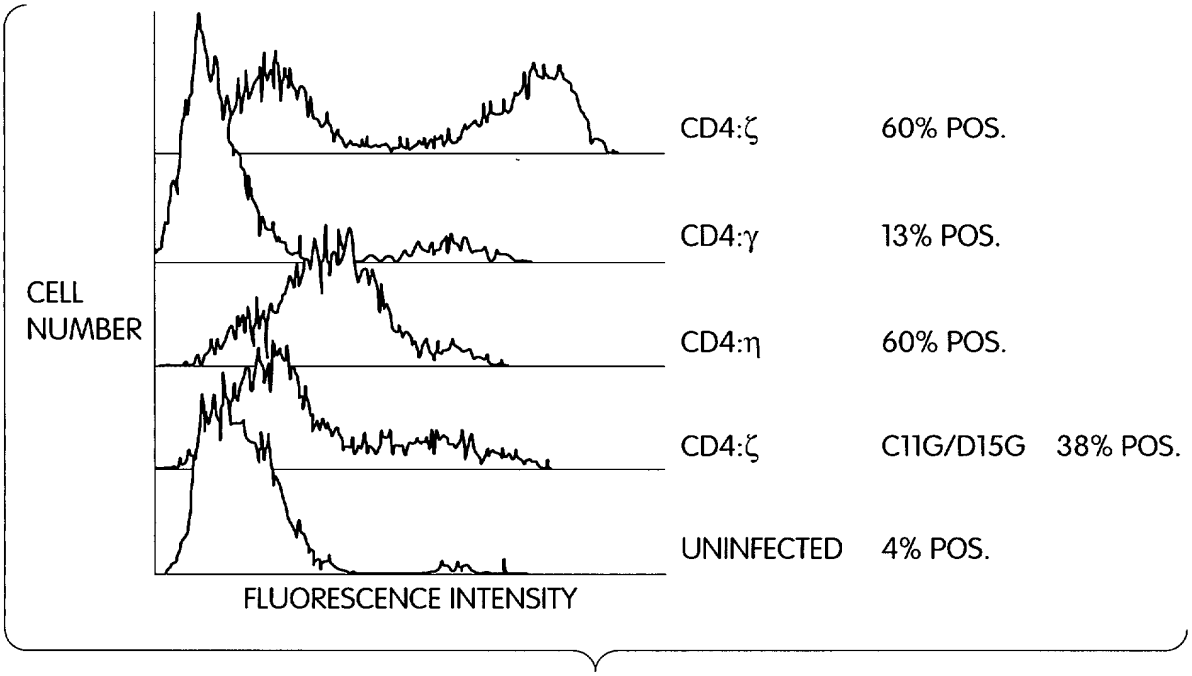
CELL NUMBER
CD4:ζ
60% POS.
CD4:γ
13% POS.
CD4:η
60% POS.
CD4:ζ
C11G/D15G
38% POS.
UNINFECTED
4% POS.
FLUORESCENCE INTENSITY

Fig. 5c

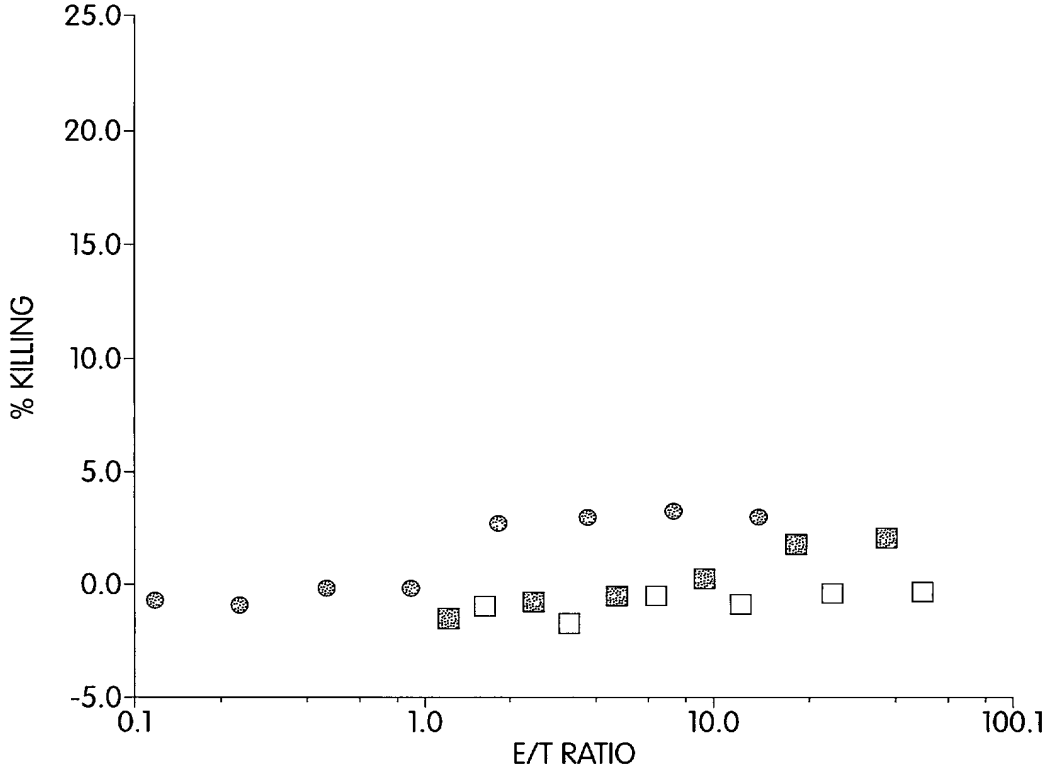
25.0
20.0
15.0
10.0
5.0
0.0
-5.0
% KILLING
0.1
1.0
10.0
100.1
E/T RATIO

Fig. 6a

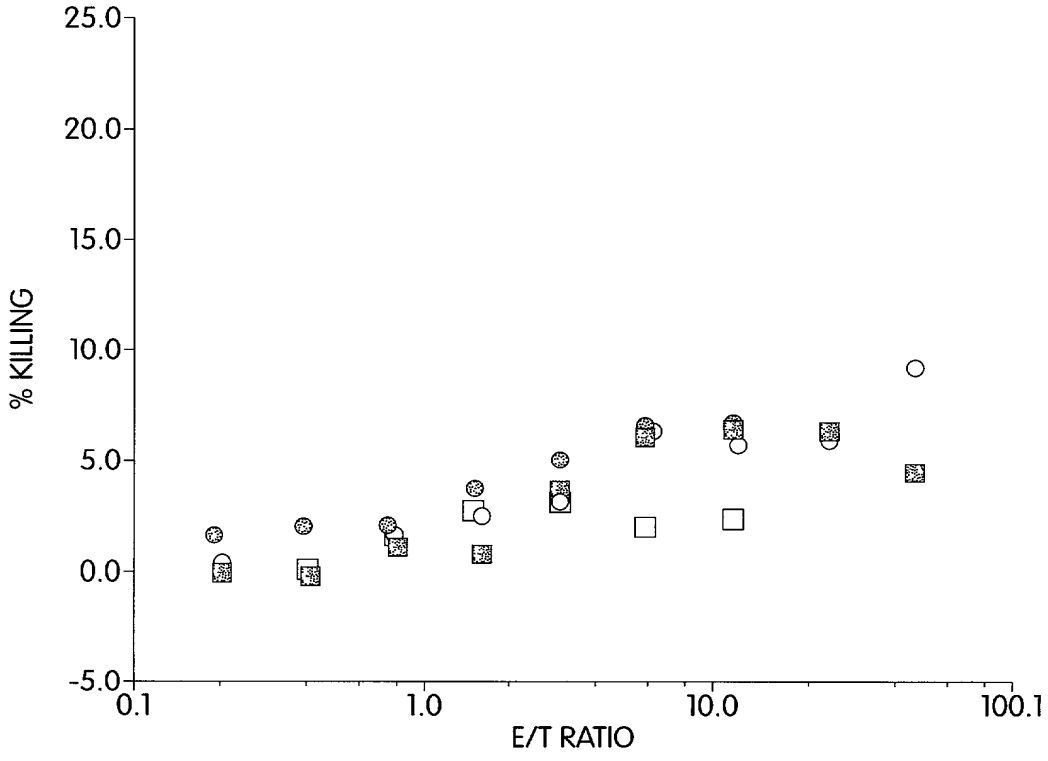
25.0
20.0
15.0
10.0
5.0
0.0
-5.0
% KILLING
0.1
1.0
10.0
100.1
E/T RATIO

Fig. 6b

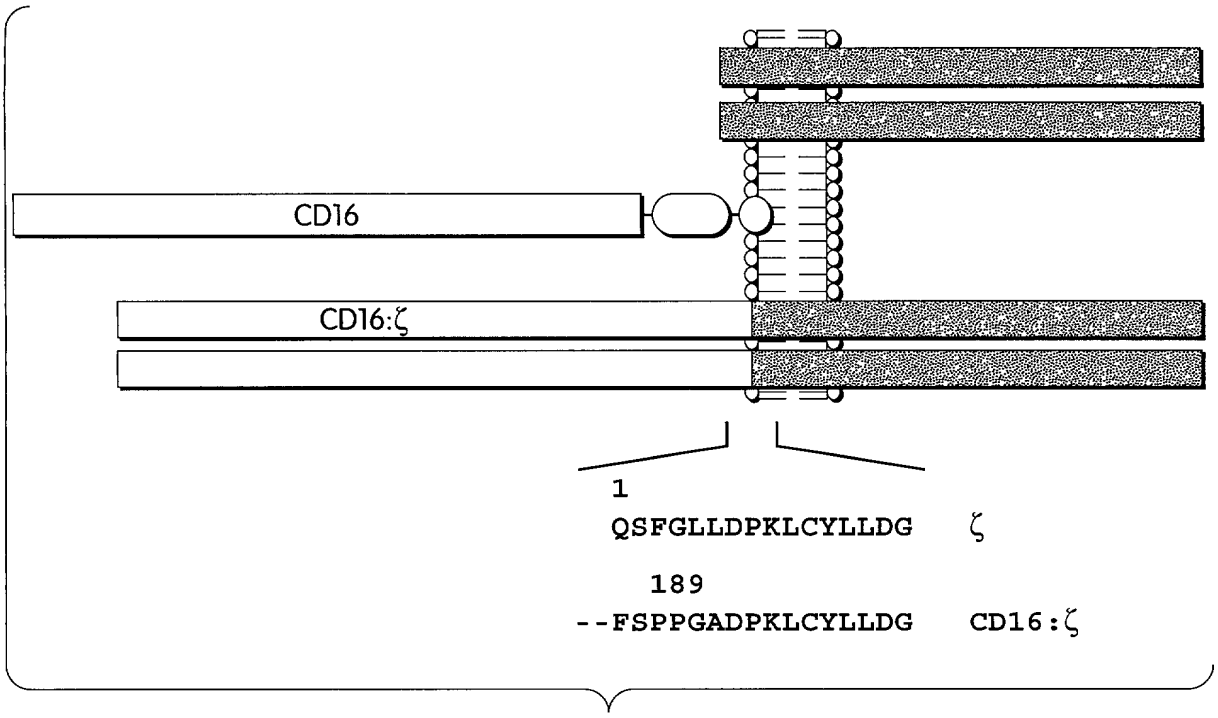
CD16
CD16:ζ
1
QSFGLLDPKLCYLLDG ζ
189
--FSPPGADPKLCYLLDG CD16:ζ

Fig. 7a

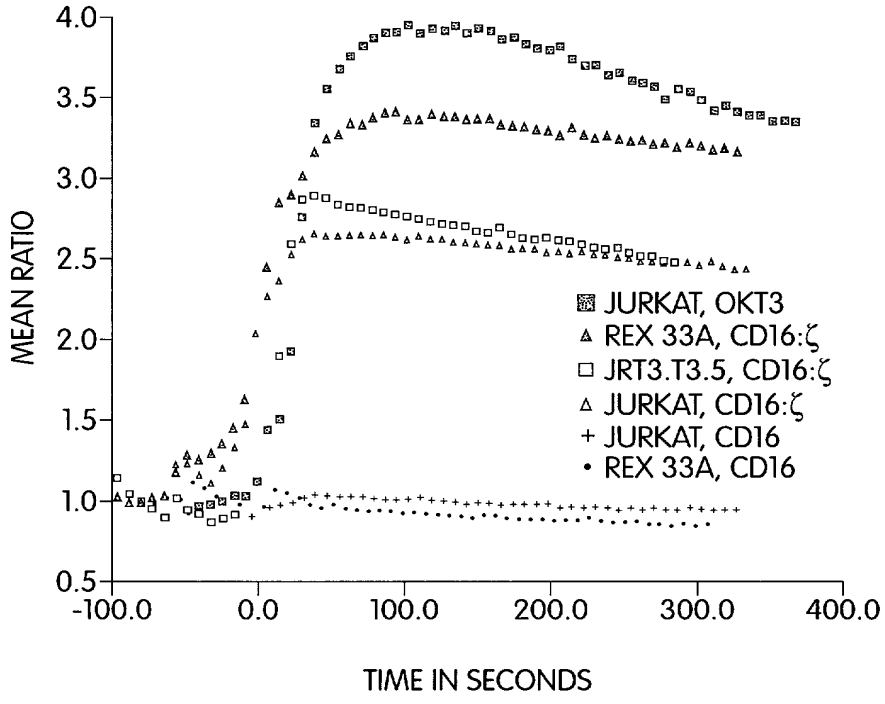
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
MEAN RATIO
-100.0
0.0
100.0
200.0
300.0
400.0
TIME IN SECONDS
JURKAT, OKT3
REX 33A, CD16:ζ
JRT3.T3.5, CD16:ζ
JURKAT, CD16:ζ
JURKAT, CD16
REX 33A, CD16

Fig. 7b

```
                                                F34*              Y51*
  1  QSFGLLDPKL CYLLDGILFI YGVILTALFL RVKFSRSAEP PAYQQGQNQL
                                                 ◄┘              ◄┘

           E60*   D66*
 51  YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQKDKMAEA
          ◄┘     ◄┘

                              G122*     A133*   L139*
101  YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR
                            ◄┘        ◄┘      ◄┘
```

Fig. 8a

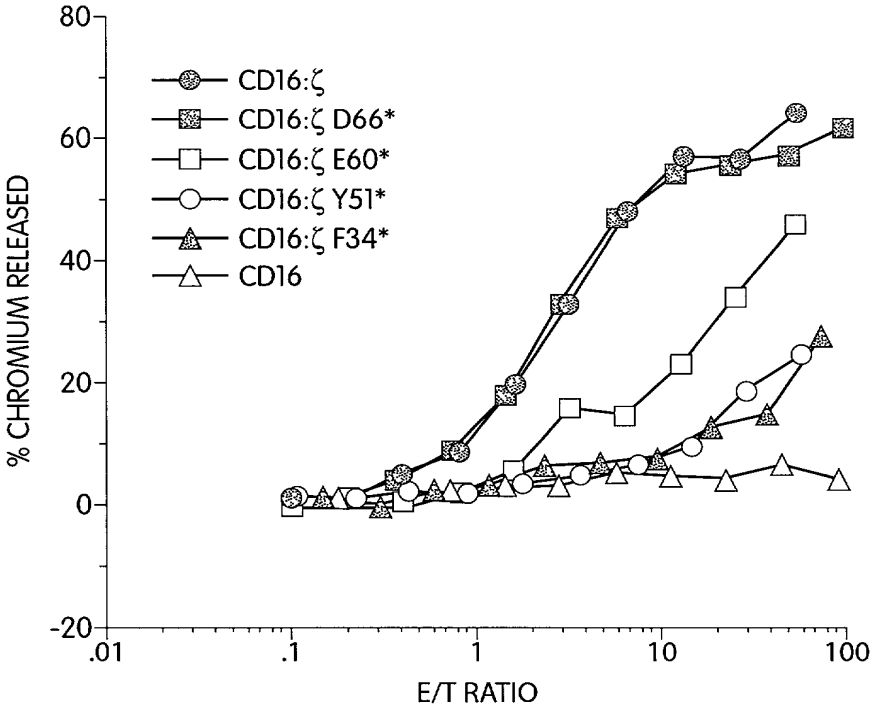

Fig. 8b

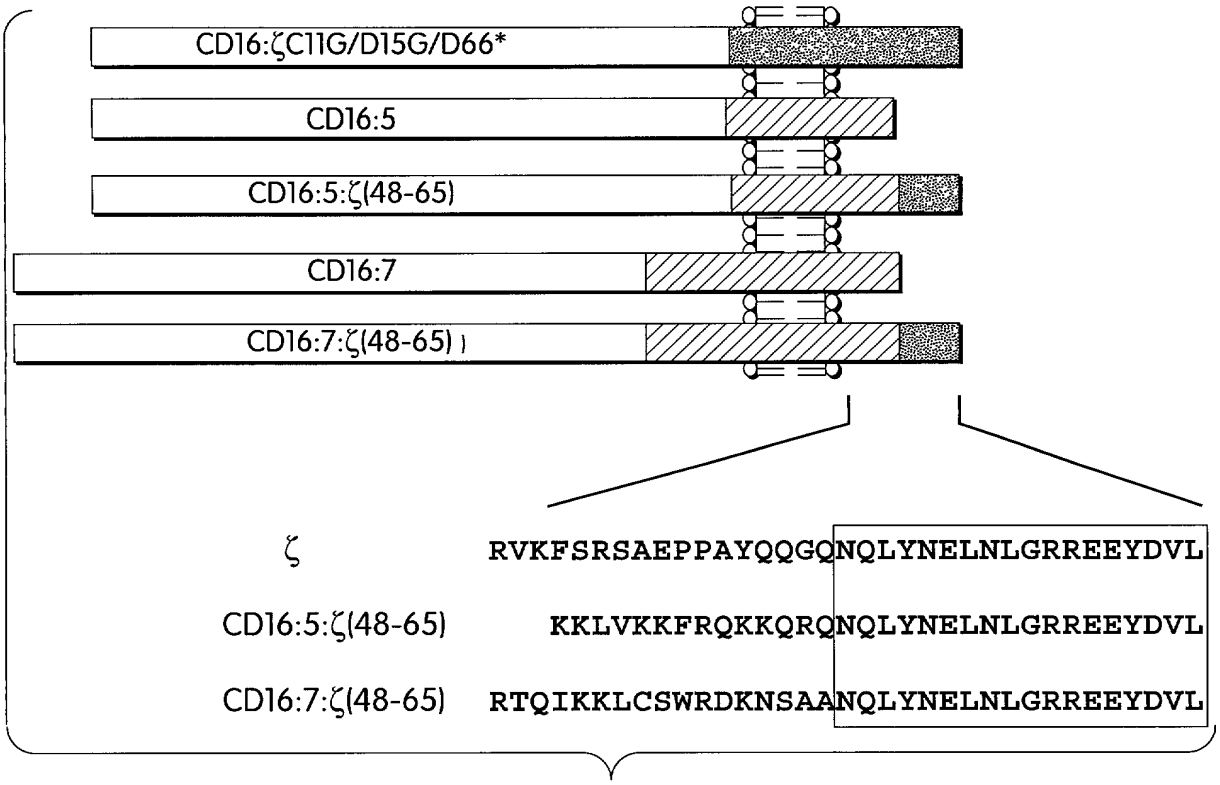
CD16:ζC11G/D15G/D66*
CD16:5
CD16:5:ζ(48-65)
CD16:7
CD16:7:ζ(48-65)
ζ RVKFSRSAEPPAYQQGQNQLYNELNLGRREEYDVL
CD16:5:ζ(48-65) KKLVKKFRQKKQRQNQLYNELNLGRREEYDVL
CD16:7:ζ(48-65) RTQIKKLCSWRDKNSAANQLYNELNLGRREEYDVL

Fig. 9a

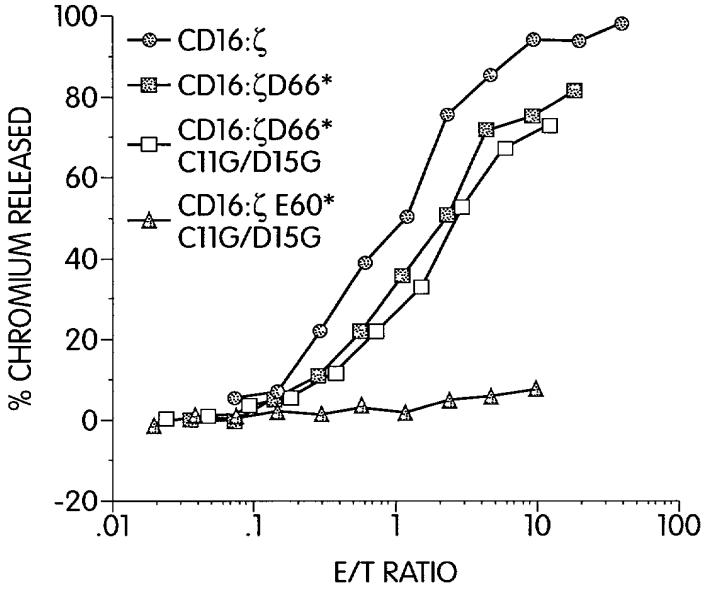
100
80
60
40
20
0
-20
% CHROMIUM RELEASED
CD16:ζ
CD16:ζD66*
CD16:ζD66* C11G/D15G
CD16:ζ E60* C11G/D15G
.01
.1
1
10
100
E/T RATIO

Fig. 9b

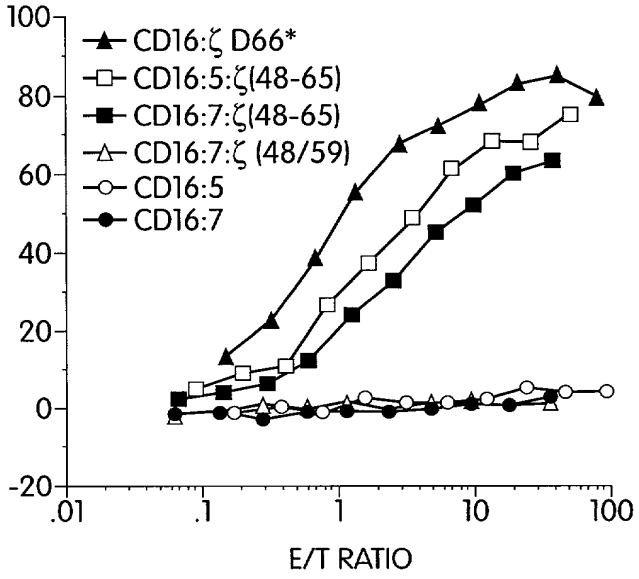
CD16:ζ D66*
CD16:5:ζ(48-65)
CD16:7:ζ(48-65)
CD16:7:ζ (48/59)
CD16:5
CD16:7
100
80
60
40
20
0
-20
.01
.1
1
10
100
E/T RATIO

Fig. 9c

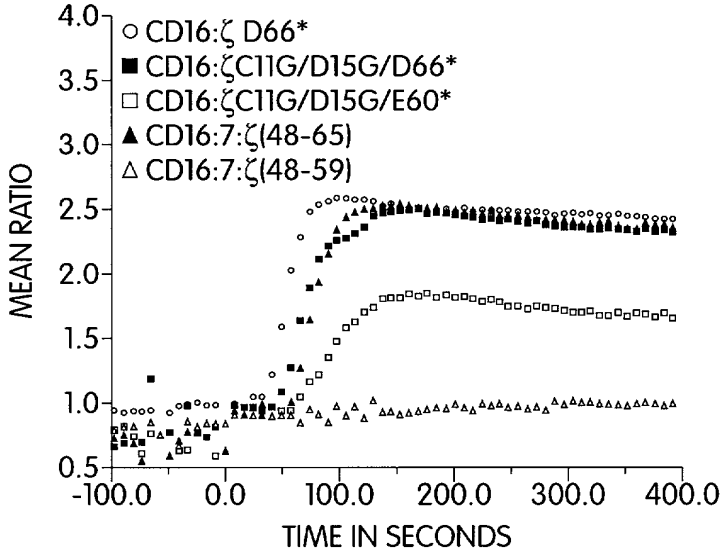
CD16:ζ D66*
CD16:ζC11G/D15G/D66*
CD16:ζC11G/D15G/E60*
CD16:7:ζ(48-65)
CD16:7:ζ(48-59)
MEAN RATIO
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
-100.0
0.0
100.0
200.0
300.0
400.0
TIME IN SECONDS

Fig. 9d

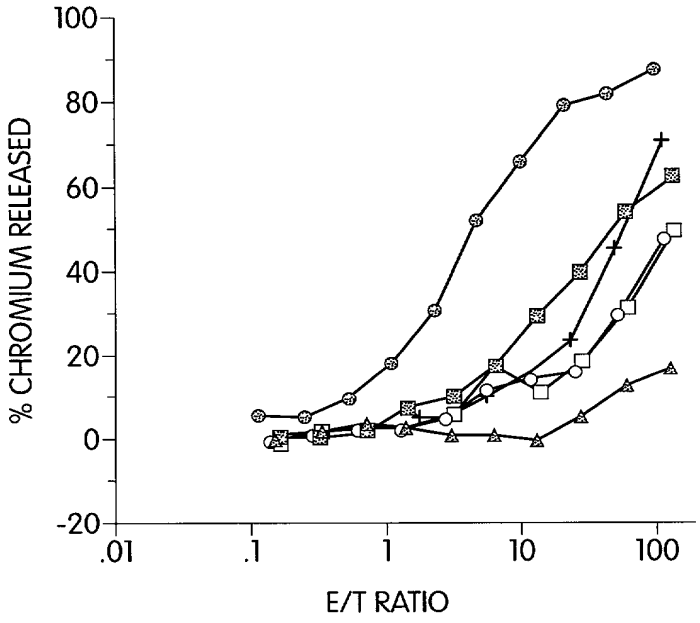

Fig. 10a

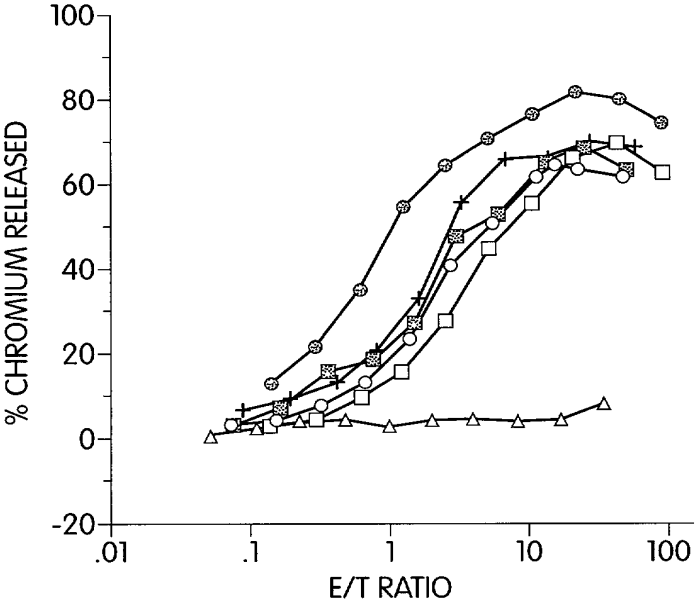

Fig. 10b

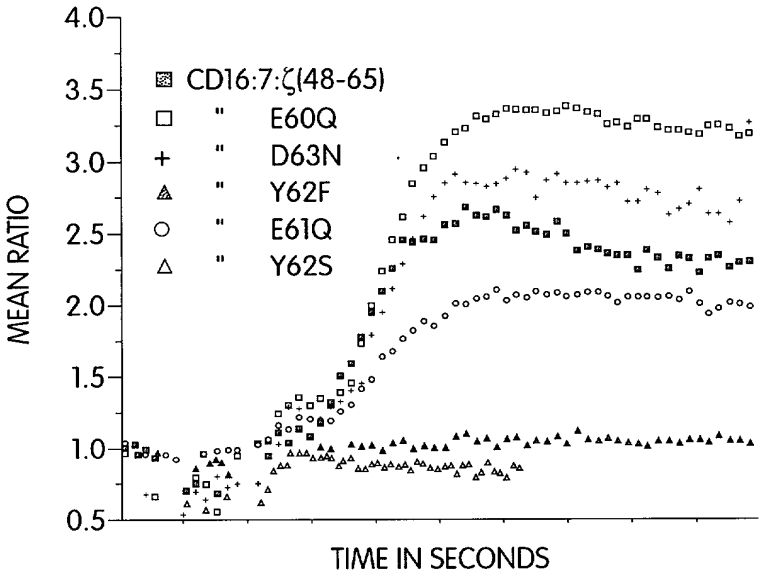

Fig. 10c

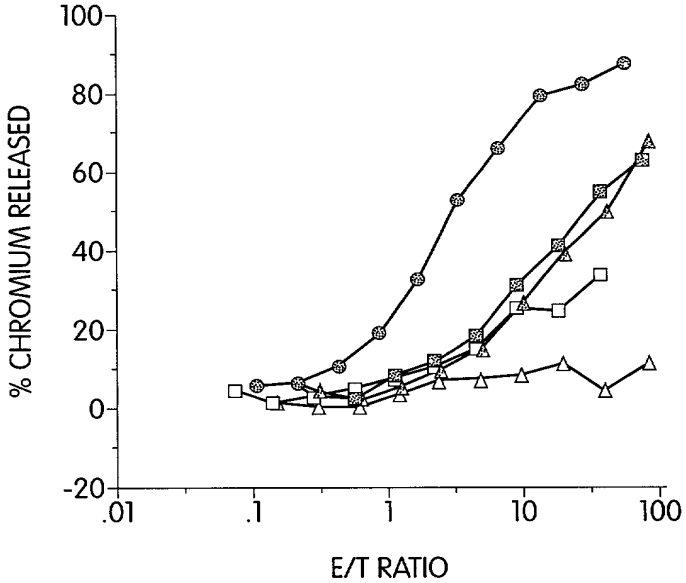

Fig. 10d

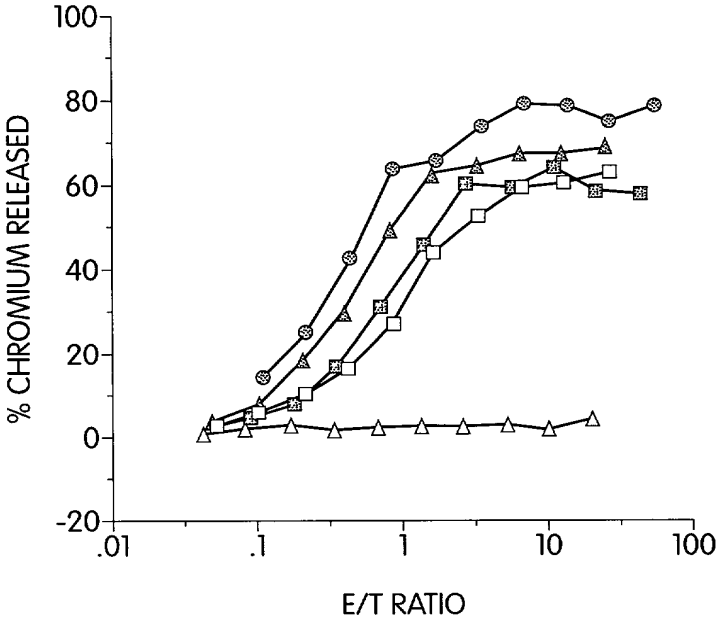

Fig. 10e

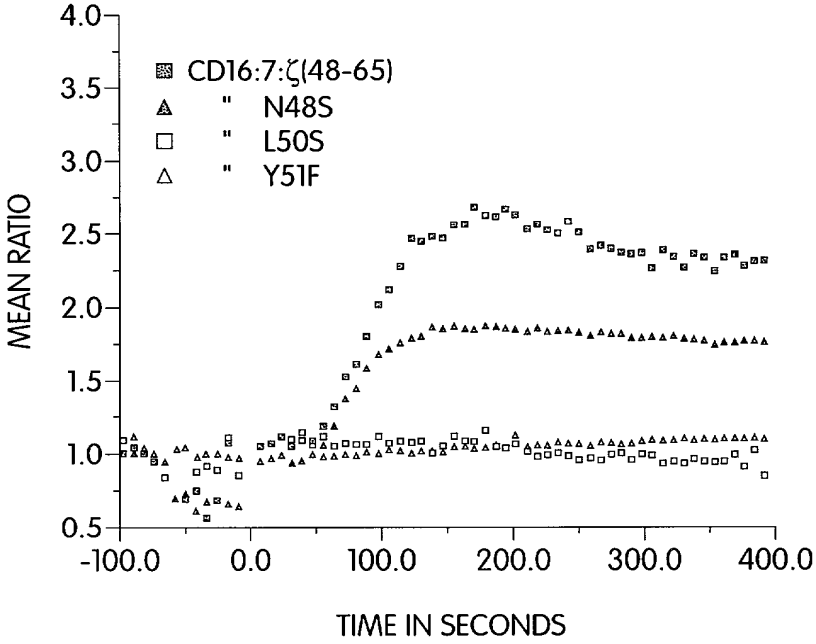

Fig. 10f

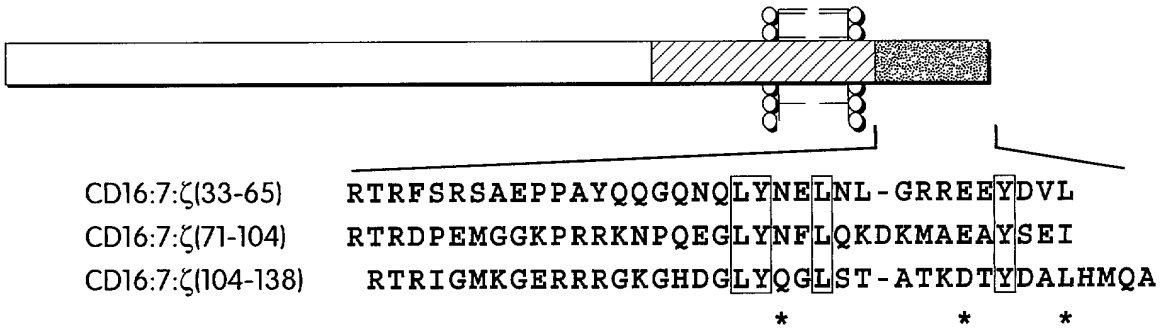

Fig. 11a

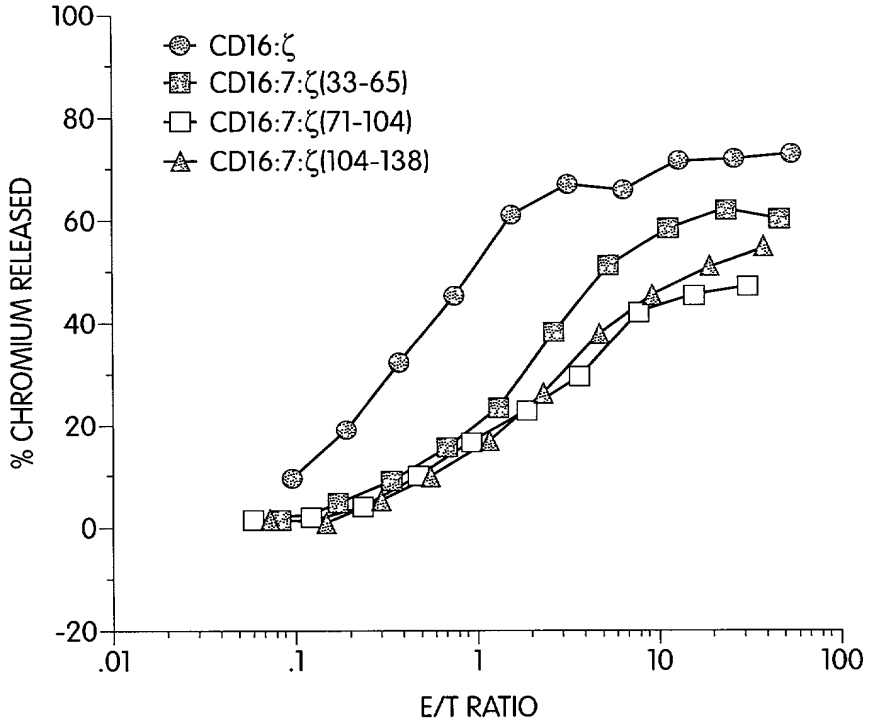

Fig. 11b

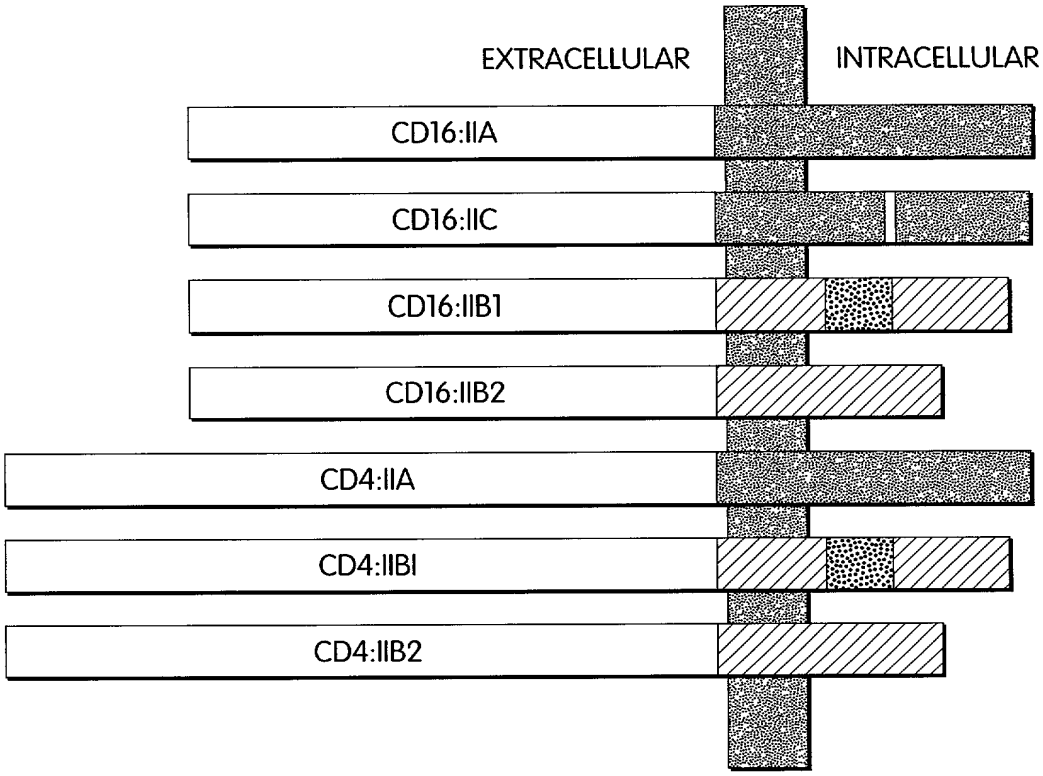
EXTRACELLULAR
INTRACELLULAR
CD16:IIA
CD16:IIC
CD16:IIB1
CD16:IIB2
CD4:IIA
CD4:IIBI
CD4:IIB2

Fig. 12

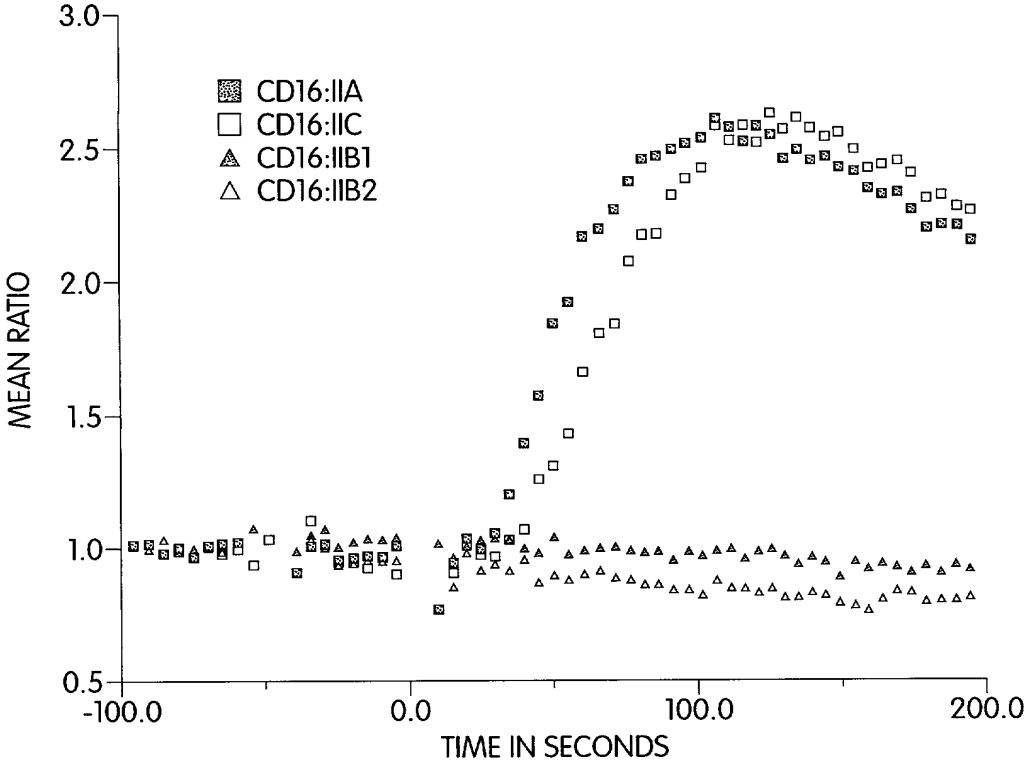

Fig. 13a

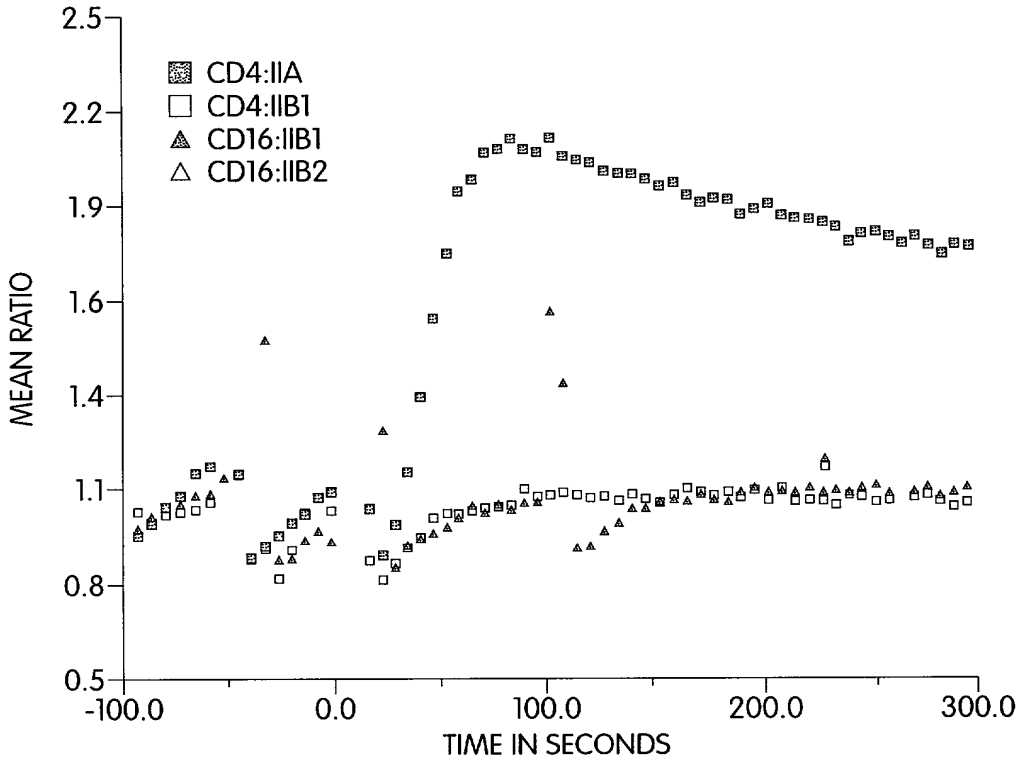

Fig. 13b

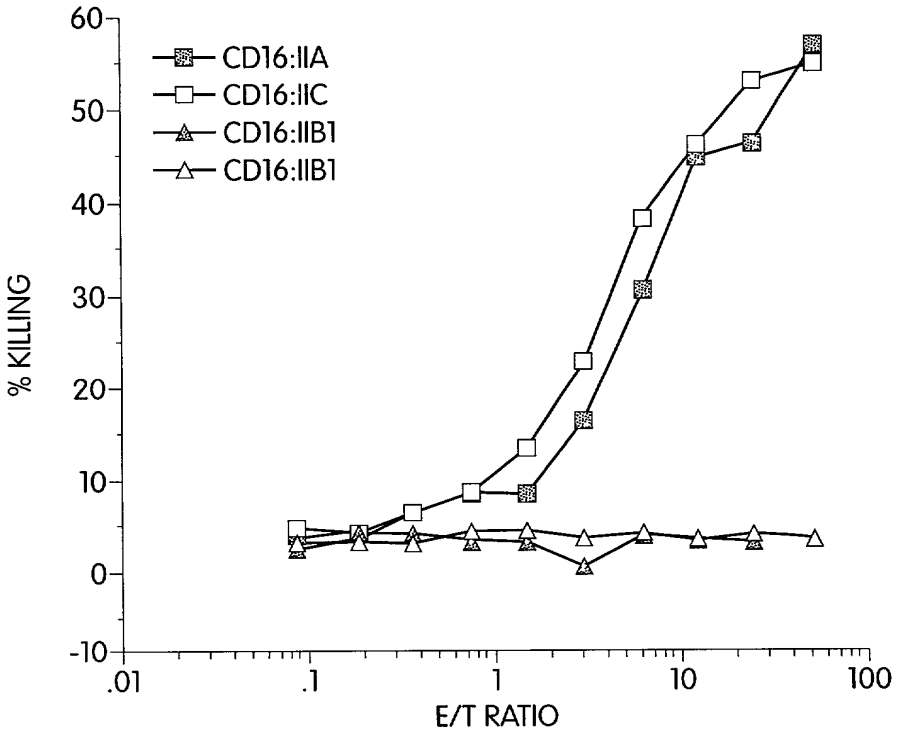

Fig. 14a

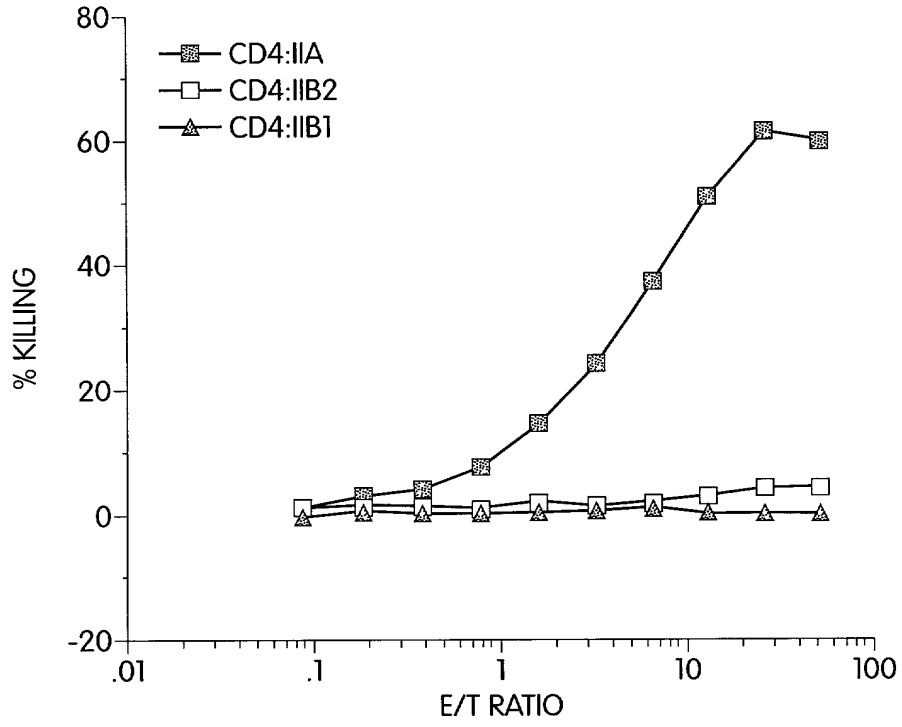

Fig. 14b

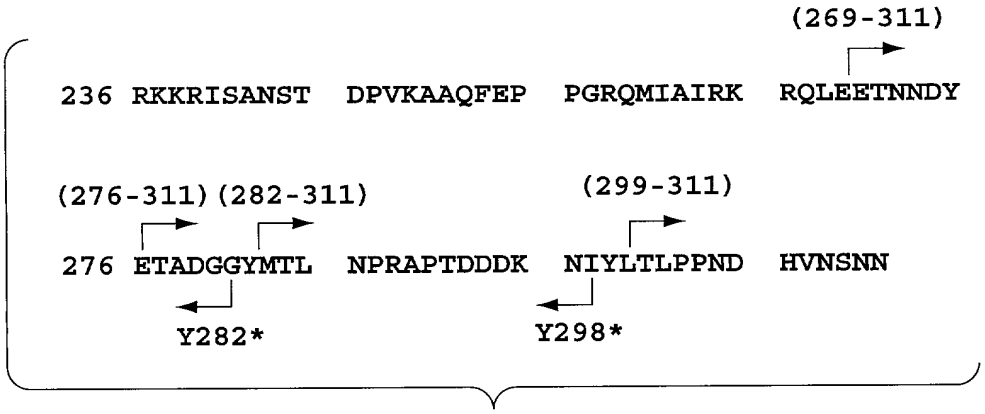

Fig. 15a

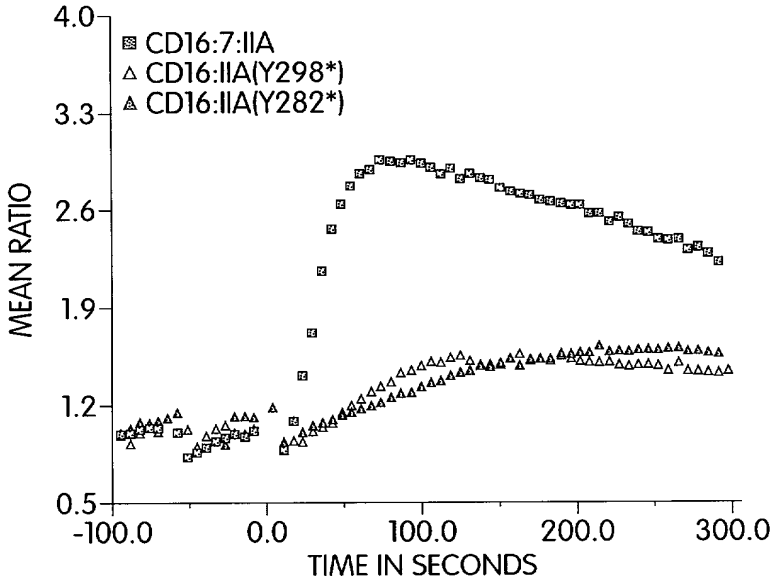

Fig. 15b

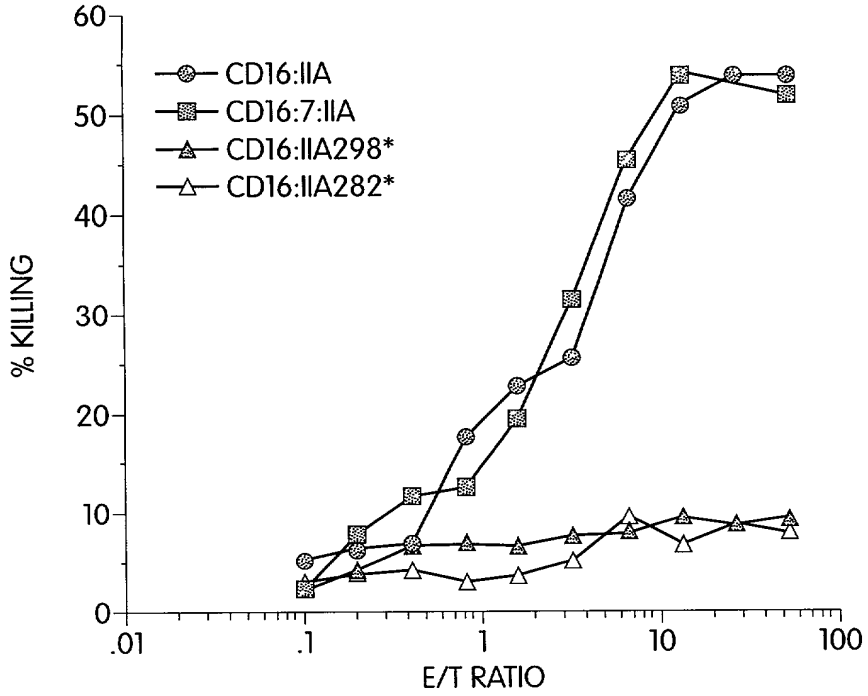

Fig. 15c

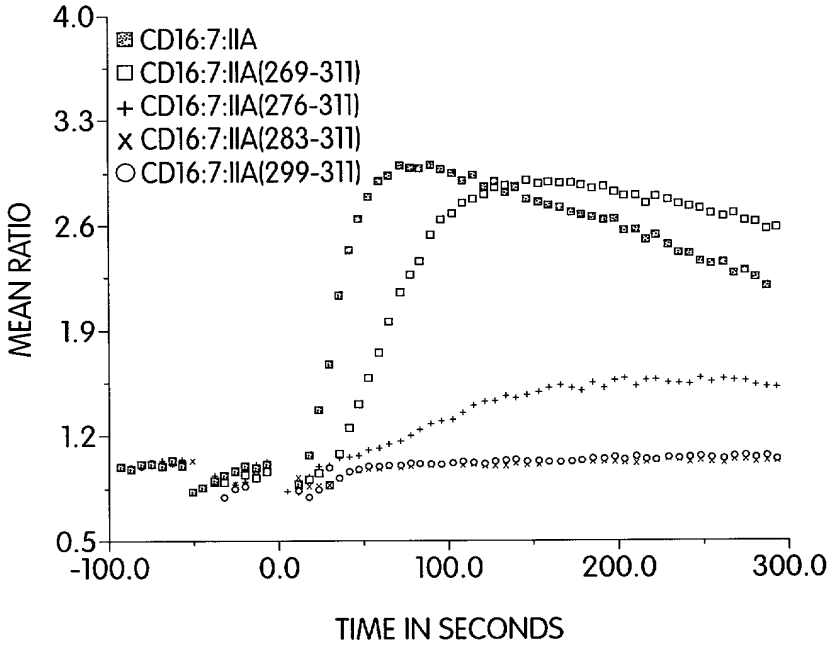

Fig. 15d

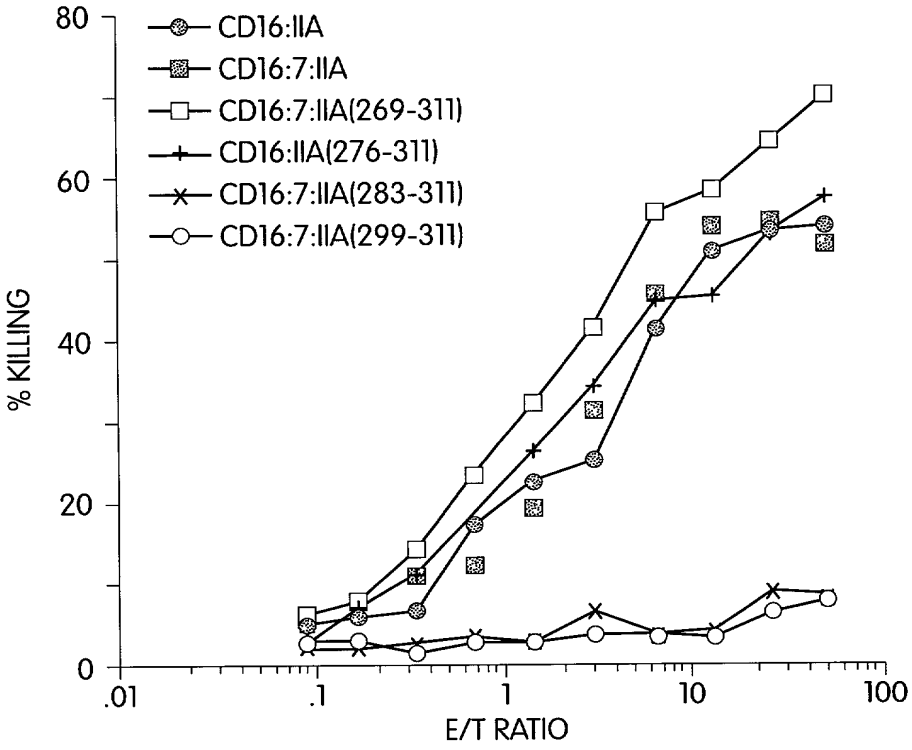
80
60
40
20
0
% KILLING
.01
.1
1
10
100
E/T RATIO
CD16:IIA
CD16:7:IIA
CD16:7:IIA(269-311)
CD16:IIA(276-311)
CD16:7:IIA(283-311)
CD16:7:IIA(299-311)

Fig. 15e

(Seq. ID No: 24)

```
1    MEHSTFLSGL  VLATLLSQVS  PFKIPIEELE  DRVFVNCNTS  ITWVEGTVGT
51   LLSDITRLDL  GKRILDPRGI  YRCNGTDIYK  DKESTVQVHY  RMCQSCVEID
101  PATVAGIIVT  DVIATLLLAL  GVFCFAGHET  GRLSGAADTQ  ALLRNDQVYQ
151  PLRDRDDAQY  SHLGGNWARN  K*
```

Fig. 16

Seq ID NO: 25)

```
1    MEQGKGLAVL  ILAIILLQGT  LAQSIKGNHL  VKVYDYQEDG  SVLLTCDAEA
51   KNITWFKDGK  MIGFLTEDKK  KWNLGSNAKD  PRGMYQCKGS  QNKSKPLQVY
101  YRMCQNCIEL  NAATISGFLF  AEIVSIFVLA  VGVYFIAGQD  GVRQSRASDK
151  QTLLPNDQLY  QPLKDREDDQ  YSHLQGNQLR  RN*
```

Fig. 17

(Seq ID No: 26)

```
1    MPGGLEALRA  LPLLLFLSYA  CLGPGCQALR  VEGGPPSLTV  NLGEEARLTC
51   ENNGRNPNIT  WWFSLQSNIT  WPPVPLGPGQ  GTTGQLFFPE  VNKNTGACTG
101  CQVIENNILK  RSCGTYLRVR  NPVPRPFLDM  GEGTKNRIIT  AEGIILLFCA
151  VVPGTLLLFR  KRWQNEKFGV  DMPDDYEDEN  LYEGLNLDDC  SMYEDISRGL
201  QGTYQDVGNL  HIGDAQLEKP  *
```

Fig. 18

(Seq ID No: 27)

```
1    MATLVLSSMP  CHWLLFLLLL  FSGEPVPAMT  SSDLPLNFQG  SPCSQIWQHP
51   RFAAKKRSSM  VKFHCYTNHS  GALTWFRKRG  SQQPQELVSE  EGRIVQTQNG
101  SVYTLTIQNI  QYEDNGIYFC  KQKCDSANHN  VTDSCGTELL  VLGFSTLDQL
151  KRRNTLKDGI  ILIQTLLIIL  FIIVPIFLLL  DKDDGKAGME  EDHTYEGLNI
201  DQTATYEDIV  TLRTGEVKWS  VGEHPGQE*
```

Fig. 19

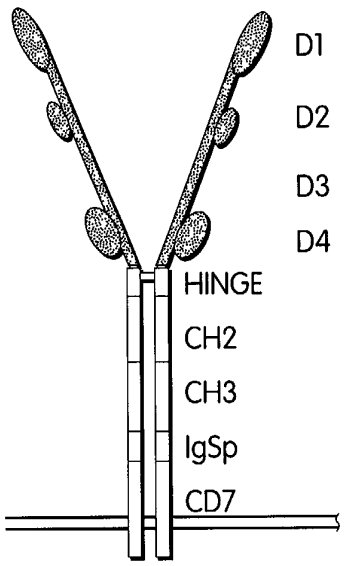

Fig. 20a

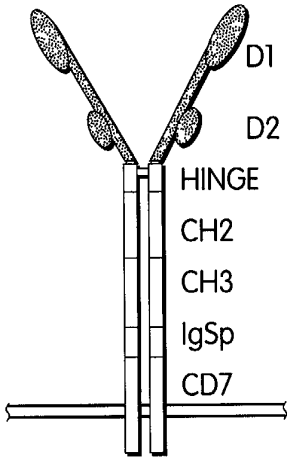

Fig. 20b

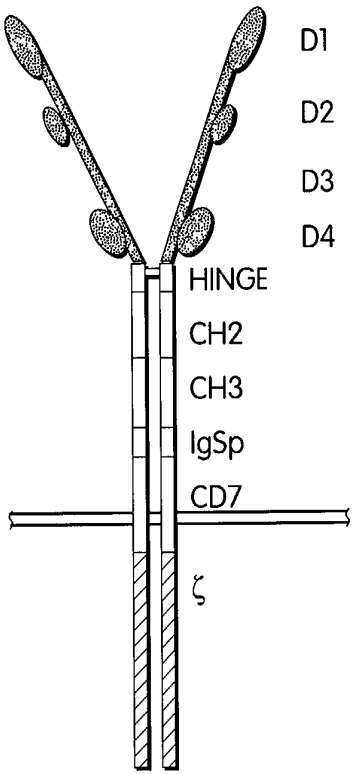

Fig. 20c

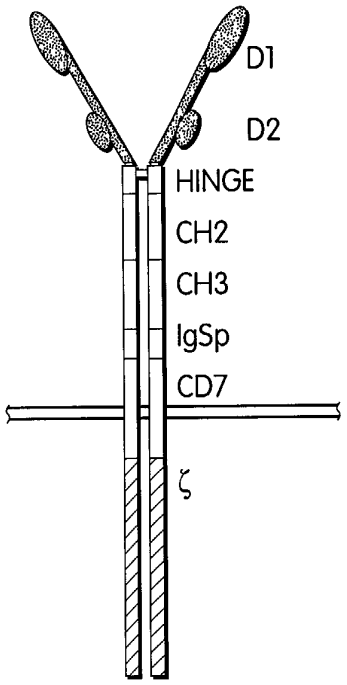

Fig. 20d

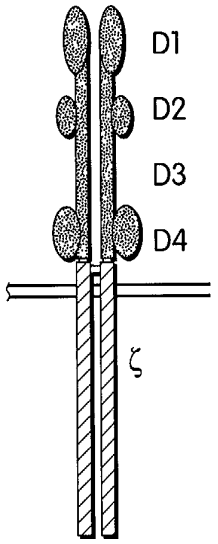

Fig. 20e

BamHI/BstY1 Bgl2/BstY1

G GAT CCC AAG GCC AGG CTA AAG CCG AAG CCG CGA AGG CCG AGG CTA AGG CCG AAG CAG ATC TG

D P K A E A K A E A K A E A K A E A D L

Fig. 28

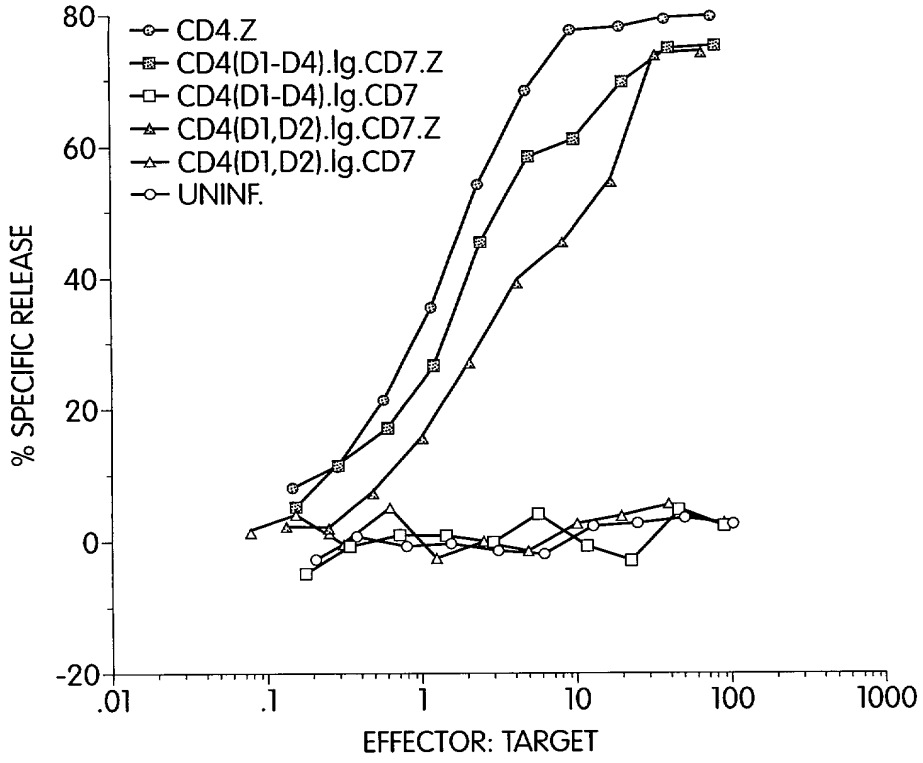
CD4.Z
CD4(D1-D4).Ig.CD7.Z
CD4(D1-D4).Ig.CD7
CD4(D1,D2).Ig.CD7.Z
CD4(D1,D2).Ig.CD7
UNINF.
% SPECIFIC RELEASE
80
60
40
20
0
-20
.01
.1
1
10
100
1000
EFFECTOR: TARGET

Fig. 21

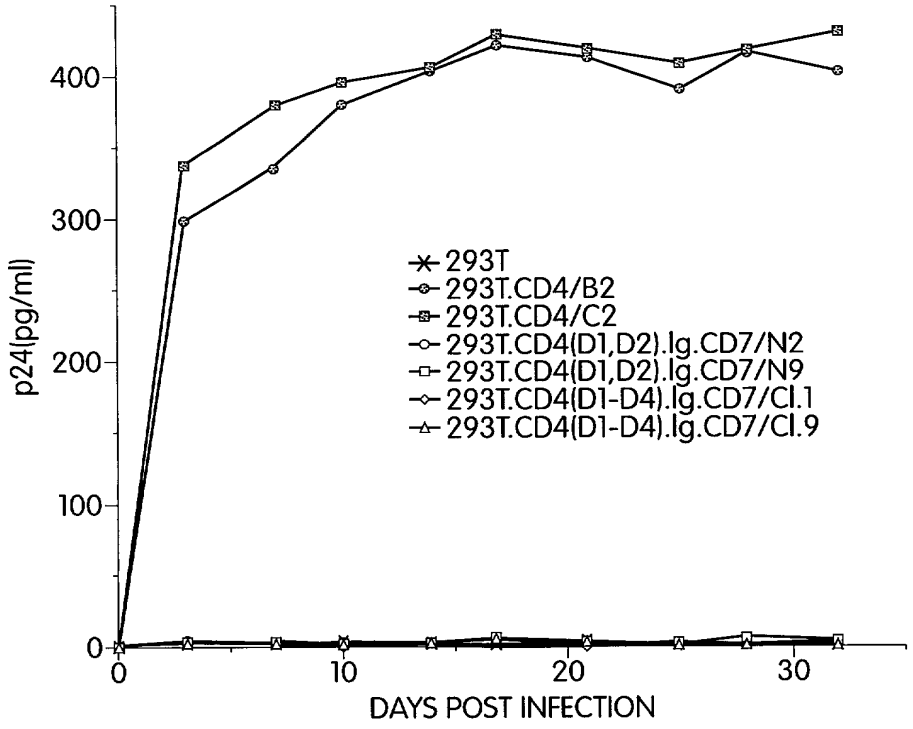
293T
293T.CD4/B2
293T.CD4/C2
293T.CD4(D1,D2).Ig.CD7/N2
293T.CD4(D1,D2).Ig.CD7/N9
293T.CD4(D1-D4).Ig.CD7/Cl.1
293T.CD4(D1-D4).Ig.CD7/Cl.9
p24(pg/ml)
400
300
200
100
0
0
10
20
30
DAYS POST INFECTION

Fig. 22

D1 - D4 of CD4

Nucleic Acid Sequence

```
GCCTGTTTGA GAAGCAGCGG GCAAGAAAGA CGCAAGCCCA GAGGCCCTGC 51
CATTTCTGTG GGCTCAGGTC CCTACTGGCT CAGGCCCCTG CCTCCCTCGG 101
CAAGGCCACA ATGAACCGGG GAGTCCCTTT TAGGCACTTG CTTCTGGTGC 151
TGCAACTGGC GCTCCTCCCA GCAGCCACTC AGGGAAACAA AGTGGTGCTG 201
GGCAAAAAAG GGGATACAGT GGAACTGACC TGTACAGCTT CCCAGAAGAA 251
GAGCATACAA TTCCACTGGA AAAACTCCAA CCAGATAAAG ATTCTGGGAA 301
ATCAGGGCTC CTTCTTAACT AAAGGTCCAT CCAAGCTGAA TGATCGCGCT 351
GACTCAAGAA GAAGCCTTTG GGACCAAGGA AACTTCCCCC TGATCATCAA 401
GAATCTTAAG ATAGAAGACT CAGATACTTA CATCTGTGAA GTGGAGGACC 451
AGAAGGAGGA GGTGCAATTG CTAGTGTTCG GATTGACTGC CAACTCTGAC 501
ACCCACCTGC TTCAGGGGCA GAGCCTGACC CTGACCTTGG AGAGCCCCCC 551
TGGTAGTAGC CCCTCAGTGC AATGTAGGAG TCCAAGGGGT AAAAACATAC 601
AGGGGGGGAA GACCCTCTCC GTGTCTCAGC TGGAGCTCCA GGATAGTGGC 651
ACCTGGACAT GCACTGTCTT GCAGAACCAG AAGAAGGTGG AGTTCAAAAT 701
AGACATCGTG GTGCTAGCTT TCCAGAAGGC CTCCAGCATA GTCTATAAGA 751
AAGAGGGGGA ACAGGTGGAG TTCTCCTTCC CACTCGCCTT TACAGTTGAA 801
AAGCTGACGG GCAGTGGCGA GCTGTGGTGG CAGGCGGAGA GGGCTTCCTC 851
CTCCAAGTCT TGGATCACCT TTGACCTGAA GAACAAGGAA GTGTCTGTAA 901
AACGGGTTAC CCAGGACCCT AAGCTCCAGA TGGGCAAGAA GCTCCCGCTC 951
CACCTCACCC TGCCCCAGGC CTTGCCTCAG TATGCTGGCT CTGGAAACCT 1001
CACCCTGGCC CTTGAAGCGA AAACAGGAAA GTTGCATCAG GAAGTGAACC 1051
TGGTGGTGAT GAGAGCCACT CAGCTCCAGA AAAATTTGAC CTGTGAGGTG 1101
TGGGGACCCA CCTCCCCTAA GCTGATGCTG AGCTTGAAAC TGGAGAACAA 1151
GGAGGCAAAG GTCTCGAAGC GGGAGAAGCC GGTGTGGGTG CTGAACCCTG 1201
AGGCGGGGAT GTGGCAGTGT CTGCTGAGTG ACTCGGGACA GGTCCTGCTG 1251
GAATCCAACA TCAAGGTTCT GCCCACATGG TCCACCCCGG TGCACGCGGA 1301
TCCC (SEQ ID NO: 28)
```

Amino Acid Sequence

```
MNRGVPFRHL LLVLQLALLP AATQGNKVVL GKKGDTVELT CTASQKKSIQ 51
FHWKNSNQIK ILGNQGSFLT KGPSKLNDRA DSRRSLWDQG NFPLIIKNLK 101
IEDSDTYICE VEDQKEEVQL LVFGLTANSD THLLQGQSLT LTLESPPGSS 151
PSVQCRSPRG KNIQGGKTLS VSQLELQDSG TWTCTVLQNQ KKVEFKIDIV 201
VLAFQKASSI VYKKEGEQVE FSFPLAFTVE KLTGSGELWW QAERASSSKS 251
WITFDLKNKE VSVKRVTQDP KLQMGKYLPL HLTLPQALPQ YAGSGNLTLA 301
LEAKTGKLHQ EVNLVVMRAT QLQKNLTCEV WGPTSPKLML SLKLENKEAK 351
VSKREKPVWV LNPEAGMWQC LLSDSGQVLL ESNIKVLPTW STPVHADP
(SEQ ID NO: 29)
```

Fig. 23

D1 - D2 of CD4

Nucleic Acid Sequence

GCCTGTTTGA GAAGCAGCGG GCAAGAAAGA CGCAAGCCCA GAGGCCCTGC 51
CATTTCTGTG GGCTCAGGTC CCTACTGGCT CAGGCCCCTG CCTCCCTCGG 101
CAAGGCCACA ATGAACCGGG GAGTCCCTTT TAGGCACTTG CTTCTGGTGC 151
TGCAACTGGC GCTCCTCCCA GCAGCCACTC AGGGAAACAA AGTGGTGCTG 201
GGCAAAAAAG GGGATACAGT GGAACTGACC TGTACAGCTT CCCAGAAGAA 251
GAGCATACAA TTCCACTGGA AAAACTCCAA CCAGATAAAG ATTCTGGGAA 301
ATCAGGGCTC CTTCTTAACT AAAGGTCCAT CCAAGCTGAA TGATCGCGCT 351
GACTCAAGAA GAAGCCTTTG GGACCAAGGA AACTTCCCCC TGATCATCAA 401
GAATCTTAAG ATAGAAGACT CAGATACTTA CATCTGTGAA GTGGAGGACC 451
AGAAGGAGGA GGTGCAATTG CTAGTGTTCG GATTGACTGC CAACTCTGAC 501
ACCCACCTGC TTCAGGGGCA GAGCCTGACC CTGACCTTGG AGAGCCCCCC 551
TGGTAGTAGC CCCTCAGTGC AATGTAGGAG TCCAAGGGGT AAAAACATAC 601
AGGGGGGGAA GACCCTCTCC GTGTCTCAGC TGGAGCTCCA GGATAGTGGC 651
ACCTGGACAT GCACTGTCTT GCAGAACCAG AAGAAGGTGG AGTTCAAAAT 701
AGACATCGTG GTGCTAGCT (SEQ ID NO: 30)

Amino Acid Sequence

MNRGVPFRHL LLVLQLALLP AATQGNKVVL GKKGDTVELT CTASQKKSIQ 51
FHWKNSNQIK ILGNQGSFLT KGPSKLNDRA DSRRSLWDQG NFPLIIKNLK 101
IEDSDTYICE VEDQKEEVQL LVFGLTANSD THLLQGQSLT LTLESPPGSS 151
PSVQCRSPRG KNIQGGKTLS VSQLELQDSG TWTCTVLQNQ KKVEFKIDIV 201
VLA (SEQ ID NO: 31)

Fig. 24

Hinge, CH2, and CH3 Domains of Human IgG1

Nucleic Acid Sequence

```
GCTAGCAGAG CCCAAATCTT GTGACAAAAC TCACACATGC CCACCGTGCC 51
CAGCACCTGA ACTCCTGGGG GGACCGTCAG TCTTCCTCTT CCCCCCAAAA 101
CCCAAGGACA CCCTCATGAT CTCCCGGACC CCTGAGGTCA CATGCGTGGT 151
GGTGGACGTG AGCCACGAAG ACCCTGAGGT CAAGTTCAAC TGGTACGTGG 201
ACGGCGTGGA GGTGCATAAT GCCAAGACAA AGCCGCGGGA GGAGCAGTAC 251
AACAGCACGT ACCGGGTGGT CAGCGTCCTC ACCGTCCTGC ACCAGGACTG 301
GCTGAATGGC AAGGAGTACA AGTGCAAGGT CTCCAACAAA GCCCTCCCAG 351
CCCCCATCGA GAAAACCATC TCCAAAGCCA AAGGGCAGCC CCGAGAACCA 401
CAGGTGTACA CCCTGCCCCC ATCCCGGGAT GAGCTGACCA AGAACCAGGT 451
CAGCCTGACC TGCCTGGTCA AAGGCTTCTA TCCCAGCGAC ATCGCCGTGG 501
AGTGGGAGAG CAATGGGCAG CCGGAGAACA ACTACAAGAC CACGCCTCCC 551
GTGCTGGACT CCGACGGCTC CTTCTTCCTC TACAGCAAGC TCACCGTGGA 601
CAAGAGCAGG TGGCAGCAGG GGAACGTCTT CTCATGCTCC GTGATGCATG 651
AGGCTCTGCA CAACCACTAC ACGCAGAAGA GCCTCTCCCT GTCTCCGGGG 701
CTGCAACTGG ACGAGACCTG TGCTGAGGCC CAGGACGGGG AGCTGGACGG 751
GCTCTGGACG ACGGATCC  (SEQ ID NO: 32)
```

Amino Acid Sequence

```
EPKSCDKTHT CPPCPAPELL GGPSVFLFPP KPKDTLMISR TPEVTCVVVD 51
VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN 101
GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR DELTKNQVSL 151
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 201
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GLQLDETCAE AQDGELDGLW 251
TTDP (SEQ ID NO: 33)
```

Fig. 25

CD7 Transmembrane Domain

Nucleic Acid Sequence

CCAAGGGCCT CTGCCCTCCC TGCCCCACCG ACAGGCTCCG CCCTCCCTGA 51
CCCGCAGACA GCCTCTGCCC TCCCTGACCC GCCAGCAGCC TCTGCCCTCC 101
CTGCGGCCCT GGCGGTGATC TCCTTCCTCC TCGGGCTGGG CCTGGGGGTG 151
GCGTGTGTGC TGGCGAGGAC GCGT (SEQ ID NO: 34)

Amino Acid Sequence

PRASALPAPP TGSALPDPQT ASALPDPPAA SALPAALAVI SFLLGLGLGV 51
ACVLARTR (SEQ.ID NO: 35)

Fig. 26

Zeta Intracellular Domain

Nucleic Acid Sequence

ACGCGTTTCA GCAGGAGCGC AGAGCCCCCC GCGTACCAGC AGGGCCAGAA 51
CCAGCTCTAT AACGAGCTCA ATCTAGGACG AAGAGAGGAG TACGATGTTT 101
TGGACAAGAG ACGTGGCCGG GACCCTGAGA TGGGGGGAAA GCCGAGAAGG 151
AAGAACCCTC AGGAAGGCCT GTACAATGAA CTGCAGAAAG ATAAGATGGC 201
GGAGGCCTAC AGTGAGATTG GGATGAAAGG CGAGCGCCGG AGGGGCAAGG 251
GGCACGATGG CCTTTACCAG GGTCTCAGTA CAGCCACCAA GGACACCTAC 301
GACGCCCTTC ACATGCAGGC CCTGCCCCCT CGCTAAAGCG GCCGC
(SEQ ID NO: 36)

Amino Acid Sequence

TRFSRSAEPP AYQQGQNQLY NELNLGRREE YDVLDKRRGR DPEMGGKPRR 51
KNPQEGLYNE LQKDKMAEAY SEIGMYGERR RGKGHDGLYO GLSTATKDTY 101
DALHMQALPP R (SEQ ID NO: 37)

Fig. 27